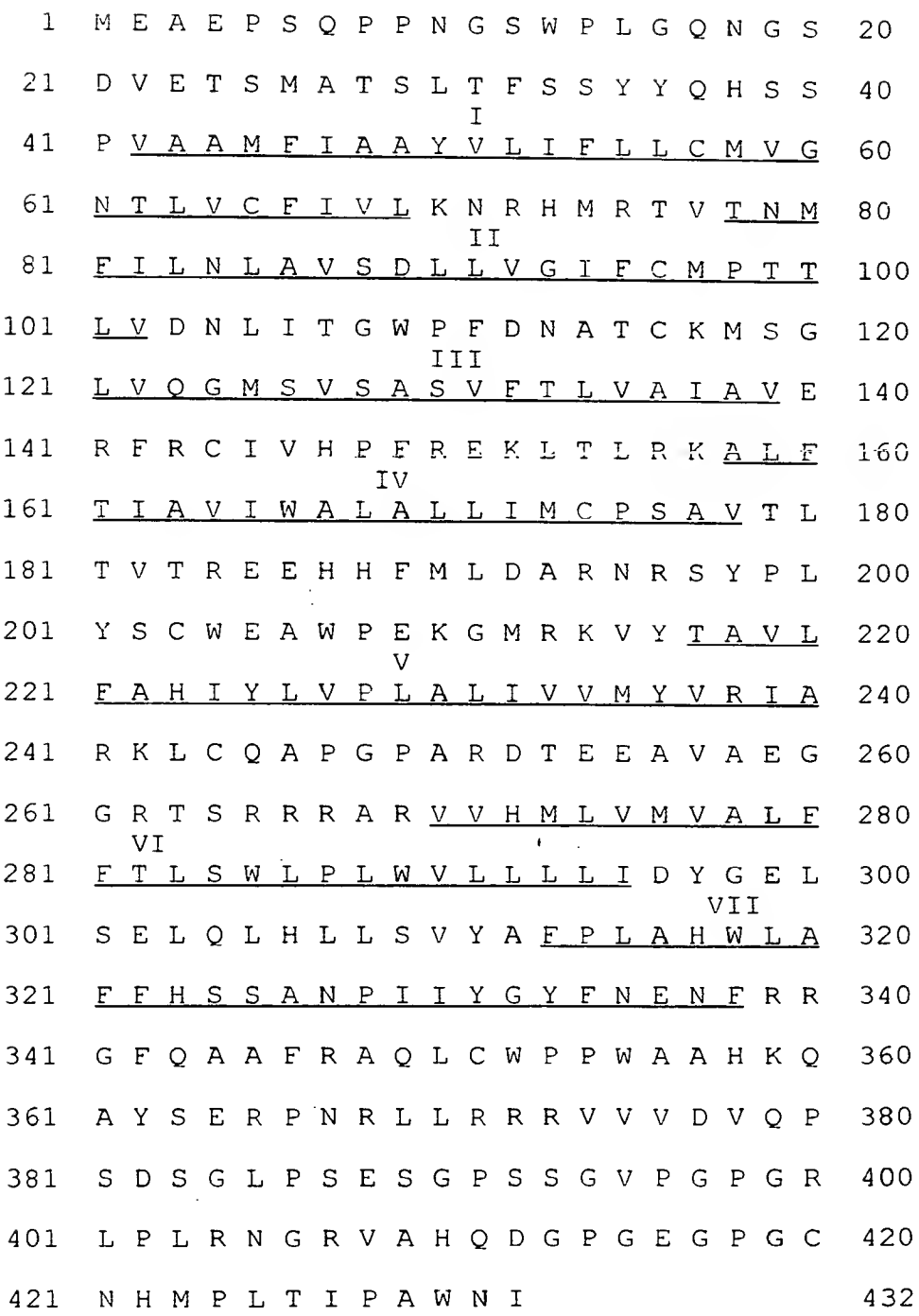
Figure 1

```
   1  ACCCTTCCTGGCCCCAGTCTACCCGCTTGAAGGTGCCCGCCTCCTTTGGAGAGTGTCCC    60
  61  GGAGCAGACAGTATGGAGGCGGAGCCCTCCCAGCCTCCCAACGGCAGCTGGCCCCTGGGT   120
 121  CAGAACGGGAGTGATGTGGAGACCAGCATGGCAACCAGCCTCACCTTCTCCTCCTACTAC   180
 181  CAACACTCCTCTCCGGTGGCAGCCATGTTCATCGCGGCCTACGTGCTCATCTTCCTCCTC   240
 241  TGCATGGTGGGCAACACCCTGGTCTGCTTCATTGTGCTCAAGAACCGGCACATGCGCACT   300
 301  GTCACCAACATGTTTATCCTCAACCTGGCCGTCAGCGACCTGCTGGTGGGCATCTTCTGC   360
 361  ATGCCCACAACCCTTGTGGACAACCTTATCACTGGTTGGCCTTTTGACAACGCCACATGC   420
 421  AAGATGAGCGGCTTGGTGCAGGGCATGTCCGTGTCTGCATCGGTTTTCACACTGGTGGCC   480
 481  ATCGCTGTGGAAAGGTTCCGCTGCATCGTGCACCCTTTCCGCGAGAAGCTGACCCTTCGG   540
 541  AAGGCGCTGTTCACCATCGCGGTGATCTGGGCTCTGGCGCTGCTCATCATGTGTCCCTCG   600
 601  GCGGTCACTCTGACAGTCACCCGAGAGGAGCATCACTTCATGCTGGATGCTCGTAACCGC   660
 661  TCCTACCCGCTCTACTCGTGCTGGGAGGCCTGGCCCGAGAAGGGCATGCGCAAGGTCTAC   720
 721  ACCGCGGTGCTCTTCGCGCACATCTACCTGGTGCCGCTGGCGCTCATCGTAGTGATGTAC   780
 781  GTGCGCATCGCGCGCAAGCTATGCCAGGCCCCCGGTCCTGCGCGCGACACGGAGGAGGCG   840
 841  GTGGCCGAGGGTGGCCGCACTTCGCGCCGTAGGGCCCGCGTGGTGCACATGCTGGTCATG   900
 901  GTGGCGCTCTTCTTCACGTTGTCCTGGCTGCCACTCTGGGTGCTGCTGCTGCTCATCGAC   960
 961  TATGGGGAGCTGAGCGAGCTGCAACTGCACCTGCTGTCGGTCTACGCCTTCCCCTTGGCA  1020
1021  CACTGGCTGGCCTTCTTCCACAGCAGCGCCAACCCCATCATCTACGGCTACTTCAACGAG  1080
1081  AACTTCCGCCGCGGCTTCCAGGCTGCCTTCCGTGCACAGCTCTGCTGGCCTCCCTGGGCC  1140
1141  GCCCACAAGCAAGCCTACTCGGAGCGGCCCAACCGCCTCCTGCGCAGGCGGGTGGTGGTG  1200
1201  GACGTGCAACCCAGCGACTCCGGCCTGCCATCAGAGTCTGGCCCCAGCAGCGGGGTCCCA  1260
1261  GGGCCTGGCCGGCTGCCACTGCGCAATGGGCGTGTGGCCCATCAGGATGGCCCGGGGGAA  1320
1321  GGGCCAGGCTGCAACCACATGCCCCTCACCATCCCGGCCTGGAACATTTGAGGTGGTCCA  1380
1381  GAGAAGGGAGGGCCAGTAGTCCTGTGGCCC                                1410
```

Figure 2

1	M	E	A	E	P	S	Q	P	P	N	G	S	W	P	L	G	Q	N	G	S	20
21	D	V	E	T	S	M	A	T	S	L	T	F	S	S	Y	Y	Q	H	S	S	40
41	P	V	A	A	M	F	I	A	A	Y	V	L	I	F	L	L	C	M	V	G	60
61	N	T	L	V	C	F	I	V	L	K	N	R	H	M	R	T	V	T	N	M	80
81	F	I	L	N	L	A	V	S	D	L	L	V	G	I	F	C	M	P	T	T	100
101	L	V	D	N	L	I	T	G	W	P	F	D	N	A	T	C	K	M	S	G	120
121	L	V	Q	G	M	S	V	S	A	S	V	F	T	L	V	A	I	A	V	E	140
141	R	F	R	C	I	V	H	P	F	R	E	K	L	T	L	R	K	A	L	F	160
161	T	I	A	V	I	W	A	L	A	L	L	I	M	C	P	S	A	V	T	L	180
181	T	V	T	R	E	E	H	H	F	M	L	D	A	R	N	R	S	Y	P	L	200
201	Y	S	C	W	E	A	W	P	E	K	G	M	R	K	V	Y	T	A	V	L	220
221	F	A	H	I	Y	L	V	P	L	A	L	I	V	V	M	Y	V	R	I	A	240
241	R	K	L	C	Q	A	P	G	P	A	R	D	T	E	E	A	V	A	E	G	260
261	G	R	T	S	R	R	R	A	R	V	V	H	M	L	V	M	V	A	L	F	280
281	F	T	L	S	W	L	P	L	W	V	L	L	L	L	I	D	Y	G	E	L	300
301	S	E	L	Q	L	H	L	L	S	V	Y	A	F	P	L	A	H	W	L	A	320
321	F	F	H	S	S	A	N	P	I	I	Y	G	Y	F	N	E	N	F	R	R	340
341	G	F	Q	A	A	F	R	A	Q	L	C	W	P	P	W	A	A	H	K	Q	360
361	A	Y	S	E	R	P	N	R	L	L	R	R	R	V	V	V	D	V	Q	P	380
381	S	D	S	G	L	P	S	E	S	G	P	S	S	G	V	P	G	P	G	R	400
401	L	P	L	R	N	G	R	V	A	H	Q	D	G	P	G	E	G	P	G	C	420
421	N	H	M	P	L	T	I	P	A	W	N	I									432

Figure 3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I
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61 N T L V C F I V L K N R H M R T V T N M 80
II
81 F I L N L A V S D L L V G I F C M P T T 100
101 L V D N L I T G W P F D N A T C K M S G 120
III
121 L V Q G M S V S A S V F T L V A I A V E 140
141 R F R C I V H P F R E K L T L R K A L F 160
IV
161 T I A V I W A L A L L I M C P S A V T L 180
181 T V T R E E H H F M L D A R N R S Y P L 200
201 Y S C W E A W P E K G M R K V Y T A V L 220
V
221 F A H I Y L V P L A L I V V M Y V R I A 240
241 R K L C Q A P G P A R D T E E A V A E G 260
261 G R T S R R R A R V V H M L V M V A L F 280
VI
281 F T L S W L P L W V L L L L I D Y G E L 300
VII
301 S E L Q L H L L S V Y A F P L A H W L A 320
321 F F H S S A N P I I Y G Y F N E N F R R 340
341 G F Q A A F R A Q L C W P P W A A H K Q 360
361 A Y S E R P N R L L R R R V V V D V Q P 380
381 S D S G L P S E S G P S S G V P G P G R 400
401 L P L R N G R V A H Q D G P G E G P G C 420
421 N H M P L T I P A W N I 432

Figure 4

```
  1  GAGCCCTCCCAGCCTCCCAACAGCAGTTGGCCCCTAAGTCAGAATGGGACTAACACTGAG   60
 61  GCCACCCCGGCTACAAACCTCACCTTCTCCTCCTACTATCAGCACACCTCCCCTGTGGCG  120
121  GCCATGTTCATTGTGGCCTATGCGCTCATCTTCCTGCTCTGCATGGTGGGCAACACCCTG  180
181  GTCTGTTTCATCGTGCTCAA                                          200
```

Figure 5

1	E	P	S	Q	P	P	N	S	S	W	P	L	S	Q	N	G	T	N	T	E	20
21	A	T	P	A	T	N	L	T	F	S	S	Y	Y	Q	H	T	S	P	V	A	40
41	A	M	F	I	V	A	Y	A	L	I	F	L	L	C	M	V	G	N	T	L	60
61	V	C	F	I	V	L															66

Figure 6

```
  1 MEAEPSQPPNGSWPLGQNGSDVETSMATSLTFSSYYQHSSPVAAMFIAAY rNPFF1
       ||||||| |||| |||.. | . ||.|||||||||.|||||||| ||
  1 ...EPSQPPNSSWPLSQNGTNTEATPATNLTFSSYYQHTSPVAAMFIVAY hNPFF1

 51 VLIFLLCMVGNTLVCFIVL                                rNPFF1
     ||||||||||||||||||
 48 ALIFLLCMVGNTLVCFIVL                                hNPFF1
```

Figure 7

```
   1  GCCGACAGGGCTCGCCGGGAGAGGTTCATCATGAATGAGAAATGGGACACAAACTCTTCA    60
  61  GAAAACTGGCATCCCATCTGGAATGTCAATGACACAAAGCATCATCTGTACTCAGATATT   120
 121  AATATTACCTATGTGAACTACTATCTTCACCAGCCTCAAGTGGCAGCAATCTTCATTATT   180
 181  TCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGTGGTTTGCTTTATTGTA   240
 241  ATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTTAAACCTGGCCATAAGT   300
 301  GATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGACAATATTATAGCAGGA   360
 361  TGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCAGGGAATATCTGTCGCA   420
 421  GCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCAGTGTGTGGTCTACCCT   480
 481  TTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTATGATCATCTGGGTCCTA   540
 541  GCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCAAGAAGAAAAATATTAC   600
 601  CGAGTGAGACTCAACTCCCAGAATAAAACCAGTCCAGTCTACTGGTGCCGGGAAGACTGG   660
 661  CCAAATCAGGAAATGAGGAAGATCTACACCACTGTGCTGTTTGCCAACATCTACCTGGCT   720
 721  CCCCTCTCCCTCATTGTCATCATGTATGGAAGGATTGGAATTTCACTCTTCAGGGCTGCA   780
 781  GTTCCTCACACAGGCAGGAAGAACCAGGAGCAGTGGCACGTGGTGTCCAGGAAGAAGCAG   840
 841  AAGATCATTAAGATGCTCCTGATTGTGGCCCTGCTTTTTATTCTCTCATGGCTGCCCCTG   900
 901  TGGACTCTAATGATGCTCTCAGACTACGCTGACCTTTCTCCAAATGAACTGCAGATCATC   960
 961  AACATCTACATCTACCCTTTTGCACACTGGCTGGCATTCGGCAACAGCAGTGTCAATCCC  1020
1021  ATCATTTATGGTTTCTTCAACGAGAATTTCCGCCGTGGTTTCCAAGAAGCTTTCCAGCTC  1080
1081  CAGCTCTGCCAAAAAAGAGCAAAGCCTATGGAAGCTTATGCCCTAAAAGCTAAAAGCCAT  1140
1141  GTGCTCATAAACACATCTAATCAGCTTGTCCAGGAATCTACATTTCAAAACCCTCATGGG  1200
1201  GAAACCTTGCTTTATAGGAAAAGTGCTGAAAAACCCCAACAGGAATTAGTGATGGAAGAA  1260
1261  TTAAAAGAAACTACTAACAGCAGTGAGATTTAAAAAGAGCTA                    1302
```

Figure 8

1	M	N	E	K	W	D	T	N	S	S	E	N	W	H	P	I	W	N	V	N	20
21	D	T	K	H	H	L	Y	S	D	I	N	I	T	Y	V	N	Y	Y	L	H	40
41	Q	P	Q	V	A	A	I	F	I	I	S	Y	F	L	I	F	F	L	C	M	60
61	M	G	N	T	V	V	C	F	I	V	M	R	N	K	H	M	H	T	V	T	80
81	N	L	F	I	L	N	L	A	I	S	D	L	L	V	G	I	F	C	M	P	100
101	I	T	L	L	D	N	I	I	A	G	W	P	F	G	N	T	M	C	K	I	120
121	S	G	L	V	Q	G	I	S	V	A	A	S	V	F	T	L	V	A	I	A	140
141	V	D	R	F	Q	C	V	V	Y	P	F	K	P	K	L	T	I	K	T	A	160
161	F	V	I	I	M	I	I	W	V	L	A	I	T	I	M	S	P	S	A	V	180
181	M	L	H	V	Q	E	E	K	Y	Y	R	V	R	L	N	S	Q	N	K	T	200
201	S	P	V	Y	W	C	R	E	D	W	P	N	Q	E	M	R	K	I	Y	T	220
221	T	V	L	F	A	N	I	Y	L	A	P	L	S	L	I	V	I	M	Y	G	240
241	R	I	G	I	S	L	F	R	A	A	V	P	H	T	G	R	K	N	Q	E	260
261	Q	W	H	V	V	S	R	K	K	Q	K	I	I	K	M	L	L	I	V	A	280
281	L	L	F	I	L	S	W	L	P	L	W	T	L	M	M	L	S	D	Y	A	300
301	D	L	S	P	N	E	L	Q	I	I	N	I	Y	I	Y	P	F	A	H	W	320
321	L	A	F	G	N	S	S	V	N	P	I	I	Y	G	F	F	N	E	N	F	340
341	R	R	G	F	Q	E	A	F	Q	L	Q	L	C	Q	K	R	A	K	P	M	360
361	E	A	Y	A	L	K	A	K	S	H	V	L	I	N	T	S	N	Q	L	V	380
381	Q	E	S	T	F	Q	N	P	H	G	E	T	L	L	Y	R	K	S	A	E	400
401	K	P	Q	Q	E	L	V	M	E	E	L	K	E	T	T	N	S	S	E	I	420

Figure 9

```
   1  M N E K W D T N S S E N W H P I W N V N  20
  21  D T K H H L Y S D I N I T Y V N Y Y L H  40
                                        I
  41  Q P Q V A A I F I I S Y F L I F F L C M  60
  61  M G N T V V C F I V M R N K H M H T V T  80
                          II
  81  N L F I L N L A I S D L L V G I F C M P 100
 101  I T L L D N I I A G W P F G N T M C K I 120
                                    III
 121  S G L V Q G I S V A A S V F T L V A I A 140
 141  V D R F Q C V V Y P F K P K L T I K T A 160
                          IV
 161  F V I I M I I W V L A I T I M S P S A V 180
 181  M L H V Q E E K Y Y R V R L N S Q N K T 200
 201  S P V Y W C R E D W P N Q E M R K I Y T 220
                          V
 221  T V L F A N I Y L A P L S L I V I M Y G 240
 241  R I G I S L F R A A V P H T G R K N Q E 260
 261  Q W H V V S R K K Q K I I K M L L I V A 280
          VI
 281  L L F I L S W L P L W T L M M L S D Y A 300
 301  D L S P N E L Q I I N I Y I Y P F A H W 320
                              VII
 321  L A F G N S S V N P I I Y G F F N E N F 340
 341  R R G F Q E A F Q L Q L C Q K R A K P M 360
 361  E A Y A L K A K S H V L I N T S N Q L V 380
 381  Q E S T F Q N P H G E T L L Y R K S A E 400
 401  K P Q Q E L V M E E L K E T T N S S E I 420
```

Figure 10


rNPFF1 MEAEPSQPPNGSWPLGQNGSDVETSMAT..SLTFSSYYQHSSPVAAMFIA 48
hNPFF2 MNEKWDTNSSENWHPIWNVNDTKHHLYSDINITYVNYYLHQPQVAAIFII 50
rNPFF1 AYVLIFLLCMVGNTLVCFIVLKNRHMRTVTNMFILNLAVSDLLVGIFCMP 98
hNPFF2 SYFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISDLLVGIFCMP 100
rNPFF1 TTLVDNLITGWPFDNATCKMSGLVQGMSVSASVFTLVAIAVERFRCIVHP 148
hNPFF2 TTLLDNIIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAVDRFQCVVYP 150
rNPFF1 FREKLTLRKALFTIAVIWALALLIMCPSAVTLTVTREEHH.FMLDARNRS 197
hNPFF2 FKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYRVRLNSQNKT 200
rNPFF1 YPLYSCWEAWPEKGMRKVYTAVLFAHIYLVPLALIVVMYVRIARKLCQAP 247
hNPFF2 SPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLFRAA 250
rNPFF1 GPARDTEEAVAEGGRTSRRRARVVHMLVMVALFFTLSWLPLWVLLLLIDY 297
hNPFF2 VPHTGRKNQ.EQWHVVSRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDY 299
rNPFF1 GELSELQLHLLSVYAFPLAHWLAFFHSSANPIIYGYFNENFRRGFQAAFR 347
hNPFF2 ADLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAFQ 349
rNPFF1 AQLCWPPWAAHKQAYSERPNRLLRRRVVVDVQPSDSGLP.SESGPSSGVP 396
hNPFF2 LQLCQKRAKPMEAYALKAKSHVLINTSNQLVQESTFQNPHGETLLYRKSA 399
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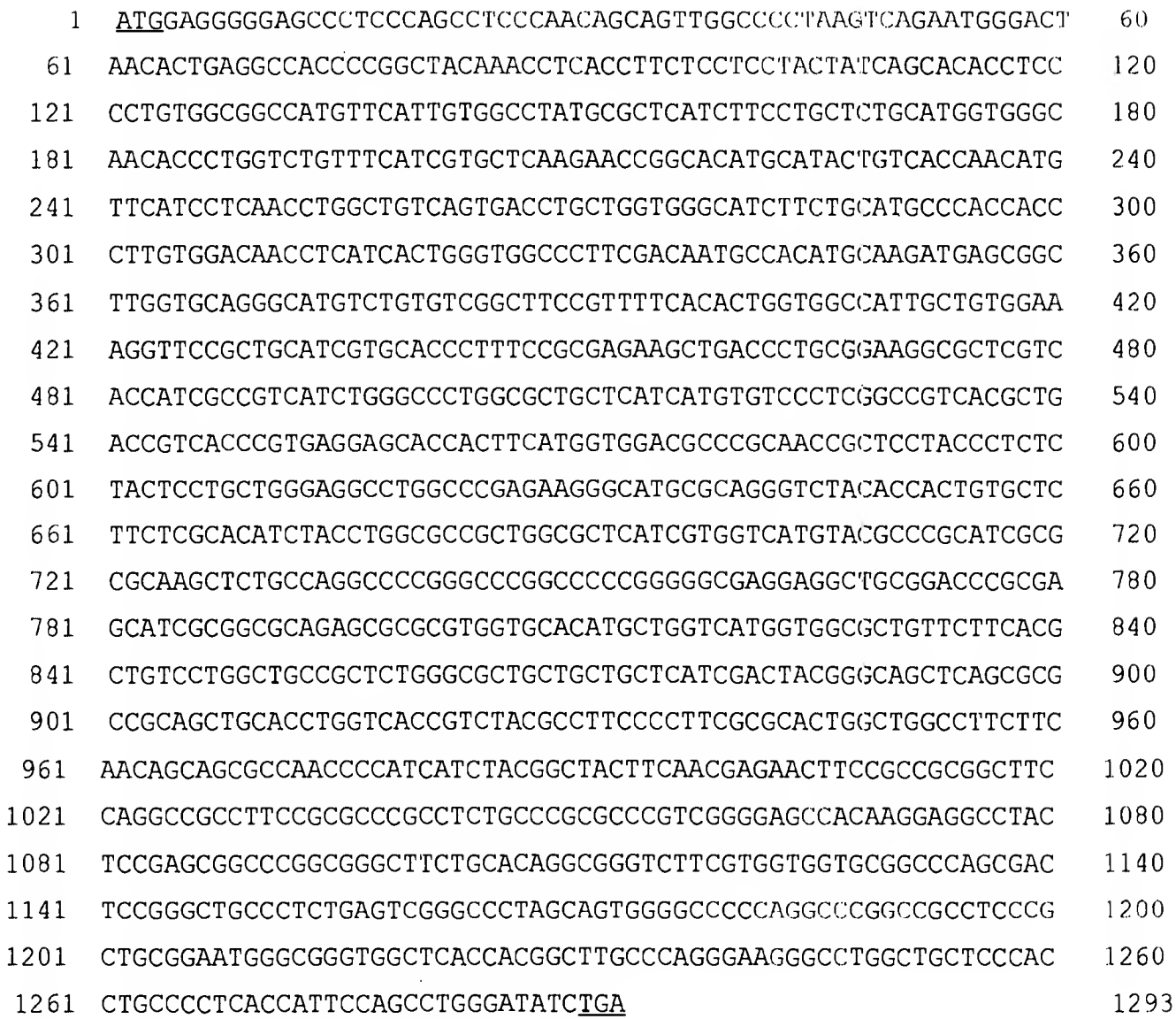
hNPFF2 EKPQQELVMEELKETTNSSEI..... 420

Figure 11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181 AACACCCTGGTCTGTTTCATCGTGCTCAAGAACCGGCACATGCATACTGTCACCAACATG 240
241 TTCATCCTCAACCTGGCTGTCAGTGACCTGCTGGTGGGCATCTTCTGCATGCCCACCACC 300
301 CTTGTGGACAACCTCATCACTGGGTGGCCCTTCGACAATGCCACATGCAAGATGAGCGGC 360
361 TTGGTGCAGGGCATGTCTGTGTCGGCTTCCGTTTTCACACTGGTGGCCATTGCTGTGGAA 420
421 AGGTTCCGCTGCATCGTGCACCCTTTCCGCGAGAAGCTGACCCTGCGGAAGGCGCTCGTC 480
481 ACCATCGCCGTCATCTGGGCCCTGGCGCTGCTCATCATGTGTCCCTCGGCCGTCACGCTG 540
541 ACCGTCACCCGTGAGGAGCACCACTTCATGGTGGACGCCCGCAACCGCTCCTACCCTCTC 600
601 TACTCCTGCTGGGAGGCCTGGCCCGAGAAGGGCATGCGCAGGGTCTACACCACTGTGCTC 660
661 TTCTCGCACATCTACCTGGCGCCGCTGGCGCTCATCGTGGTCATGTACGCCCGCATCGCG 720
721 CGCAAGCTCTGCCAGGCCCCGGGCCCGGCCCCCGGGGGCGAGGAGGCTGCGGACCCGCGA 780
781 GCATCGCGGCGCAGAGCGCGCGTGGTGCACATGCTGGTCATGGTGGCGCTGTTCTTCACG 840
841 CTGTCCTGGCTGCCGCTCTGGGCGCTGCTGCTGCTCATCGACTACGGGCAGCTCAGCGCG 900
901 CCGCAGCTGCACCTGGTCACCGTCTACGCCTTCCCCTTCGCGCACTGGCTGGCCTTCTTC 960
961 AACAGCAGCGCCAACCCCATCATCTACGGCTACTTCAACGAGAACTTCCGCCGCGGCTTC 1020
1021 CAGGCCGCCTTCCGCGCCCGCCTCTGCCCGCGCCCGTCGGGGAGCCACAAGGAGGCCTAC 1080
1081 TCCGAGCGGCCCGGCGGGCTTCTGCACAGGCGGGTCTTCGTGGTGGTGCGGCCCAGCGAC 1140
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1201 CTGCGGAATGGGCGGGTGGCTCACCACGGCTTGCCCAGGGAAGGGCCTGGCTGCTCCCAC 1260
1261 CTGCCCCTCACCATTCCAGCCTGGGATATCTGA 1293

Figure 12

1	M	E	G	E	P	S	Q	P	P	N	S	S	W	P	L	S	Q	N	G	T	20
21	N	T	E	A	T	P	A	T	N	L	T	F	S	S	Y	Y	Q	H	T	S	40
41	P	V	A	A	M	F	I	V	A	Y	A	L	I	F	L	L	C	M	V	G	60
61	N	T	L	V	C	F	I	V	L	K	N	R	H	M	H	T	V	T	N	M	80
81	F	I	L	N	L	A	V	S	D	L	L	V	G	I	F	C	M	P	T	T	100
101	L	V	D	N	L	I	T	G	W	P	F	D	N	A	T	C	K	M	S	G	120
121	L	V	Q	G	M	S	V	S	A	S	V	F	T	L	V	A	I	A	V	E	140
141	R	F	R	C	I	V	H	P	F	R	E	K	L	T	L	R	K	A	L	V	160
161	T	I	A	V	I	W	A	L	A	L	L	I	M	C	P	S	A	V	T	L	180
181	T	V	T	R	E	E	H	H	F	M	V	D	A	R	N	R	S	Y	P	L	200
201	Y	S	C	W	E	A	W	P	E	K	G	M	R	R	V	Y	T	T	V	L	220
221	F	S	H	I	Y	L	A	P	L	A	L	I	V	V	M	Y	A	R	I	A	240
241	R	K	L	C	Q	A	P	G	P	A	P	G	G	E	E	A	A	D	P	R	260
261	A	S	R	R	R	A	R	V	V	H	M	L	V	M	V	A	L	F	F	T	280
281	L	S	W	L	P	L	W	A	L	L	L	L	I	D	Y	G	Q	L	S	A	300
301	P	Q	L	H	L	V	T	V	Y	A	F	P	F	A	H	W	L	A	F	F	320
321	N	S	S	A	N	P	I	I	Y	G	Y	F	N	E	N	F	R	R	G	F	340
341	Q	A	A	F	R	A	R	L	C	P	R	P	S	G	S	H	K	E	A	Y	360
361	S	E	R	P	G	G	L	L	H	R	R	V	F	V	V	V	R	P	S	D	380
381	S	G	L	P	S	E	S	G	P	S	S	G	A	P	R	P	G	R	L	P	400
401	L	R	N	G	R	V	A	H	H	G	L	P	R	E	G	P	G	C	S	H	420
421	L	P	L	T	I	P	A	W	D	I											430

Figure 13

```
   1  M E G E P S Q P P N S S W P L S Q N G T  20

  21  N T E A T P A T N L T F S S Y Y Q H T S  40
                           I
  41  P V A A M F I V A Y A L I F L L C M V G  60

  61  N T L V C F I V L K N R H M H T V T N M  80
                       II
  81  F I L N L A V S D L L V G I F C M P T T 100

 101  L V D N L I T G W P F D N A T C K M S G 120
                       III
 121  L V Q G M S V S A S V F T L V A I A V E 140

 141  R F R C I V H P F R E K L T L R K A L V 160
                       IV
 161  T I A V I W A L A L L I M C P S A V T L 180

 181  T V T R E E H H F M V D A R N R S Y P L 200

 201  Y S C W E A W P E K G M R R V Y T T V L 220
                         V
 221  F S H I Y L A P L A L I V V M Y A R I A 240

 241  R K L C Q A P G P A P G G E E A A D P R 260
                                 VI
 261  A S R R R A R V V H M L V M V A L F F T 280

 281  L S W L P L W A L L L L I D Y G Q L S A 300

 301  P Q L H L V T V Y A F P F A H W L A F F 320
                       VII
 321  N S S A N P I I Y G Y F N E N F R R G F 340

 341  Q A A F R A R L C P R P S G S H K E A Y 360

 361  S E R P G G L L H R R V F V V V R P S D 380

 381  S G L P S E S G P S S G A P R P G R L P 400

 401  L R N G R V A H H G L P R E G P G C S H 420

 421  L P L T I P A W D I                    430
```

Figure 14


hNPFF2 1 MNEKWDTNSSENWHPIWNVNDTKHHLYSDINITYVNYYLHQPQVAAIFII 50
hNPFF1 1 ..MEGEPSQPPNSSWPLSQNGTNTEATPATNLTFSSYYQHTSPVAAMFIV 48
hNPFF2 51 SYFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISDLLVGIFCMP 100
hNPFF1 49 AYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMP 98
hNPFF2 101 ITLLDNIIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAVDRFQCVVYP 150
hNPFF1 99 TTLVDNLITGWPFDNATCKMSGLVQGMSVSASVFTLVAIAVERFRCIVHP 148
hNPFF2 151 FKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYRVRLNSQNKT 200
hNPFF1 149 FREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHH.FMVDARNRS 197
hNPFF2 201 SPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLFRAA 250
hNPFF1 198 YPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARKLCQAP 247
hNPFF2 251 VPHTGRKNQEQWHVVSRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 300
hNPFF1 248 GPAPGGEEAADPR.ASRRRARVVHMLVMVALFFTLSWLPLWALLLLIDYG 296
hNPFF2 301 DLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAFQL 350
hNPFF1 297 QLSAPQLHLVTVYAFPFAHWLAFFNSSANPIIYGYFNENFRRGFQAAFRA 346
hNPFF2 351 QLCQKRAKPMEAYALKAKSHVLINTSNQLVQESTFQNPHGETLLYRKSAE 400
hNPFF1 347 RLC.PRPSGSHKEAYSERPGGLLHRRVFVVVRPSDSGLPSESGPSSGAPR 395
hNPFF2 401 KPQQELVMEELKETTNSSEI*..... 420
hNPFF1 396 PGRLPLRNGRVAHHGLPREGPGCSHLPLTIPAWDI* 431

Figure 15A

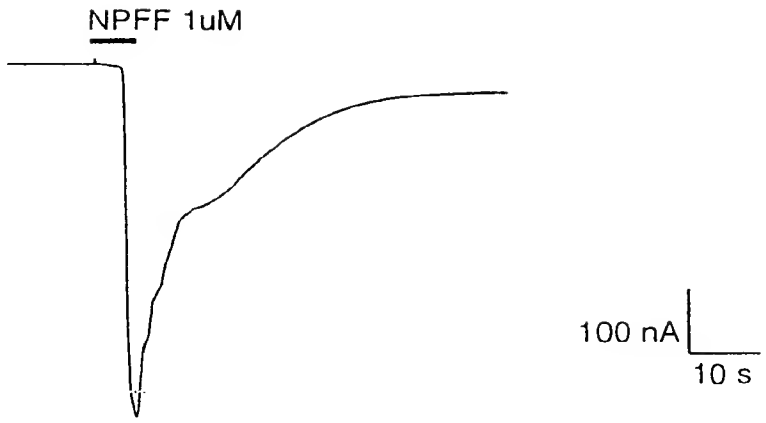


Figure 15B

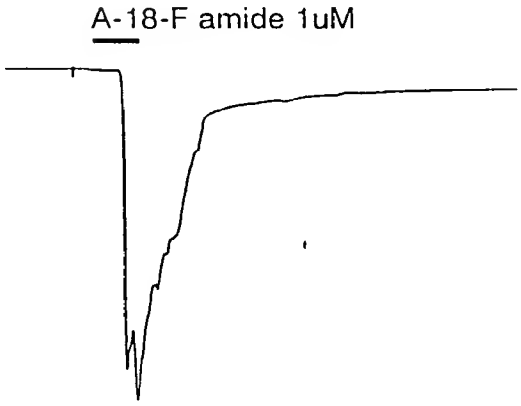


Figure 15C

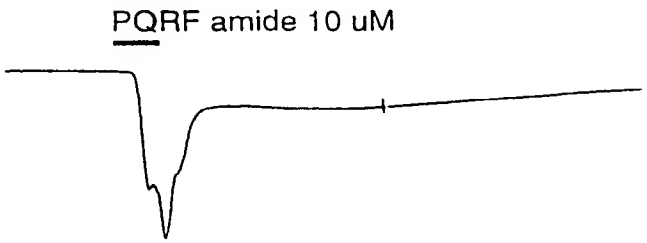


Figure 16A

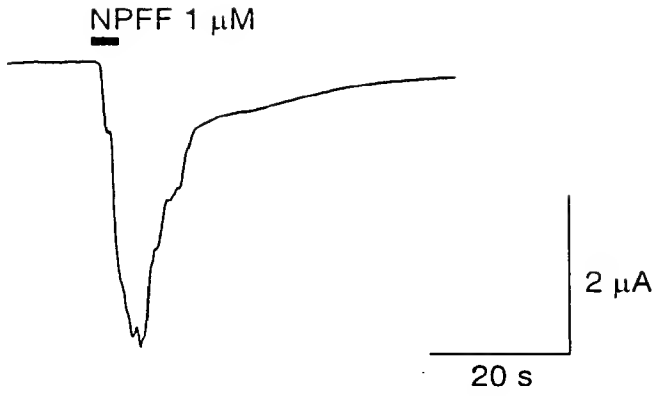


Figure 16B

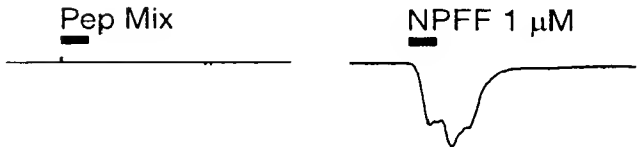


Figure 16C

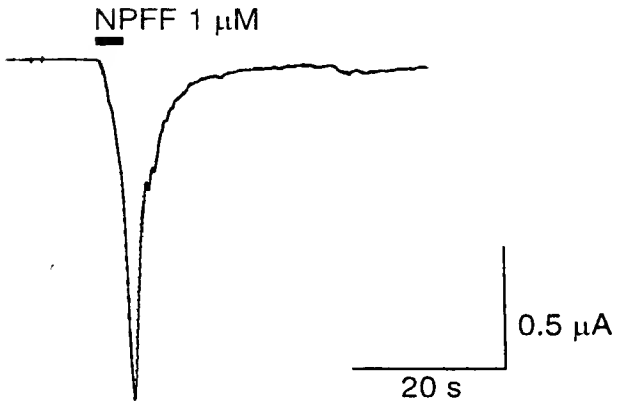


Figure 17A

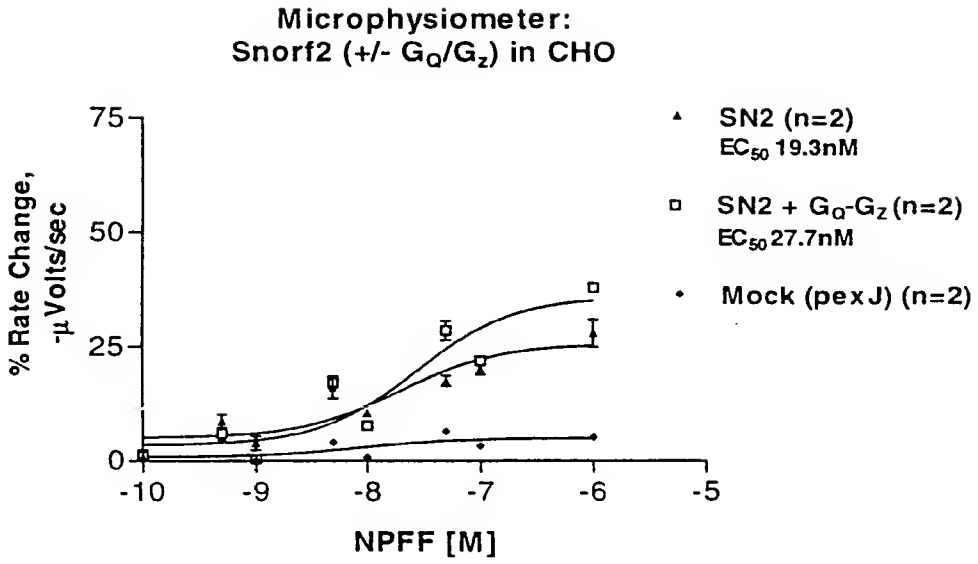


Figure 17B

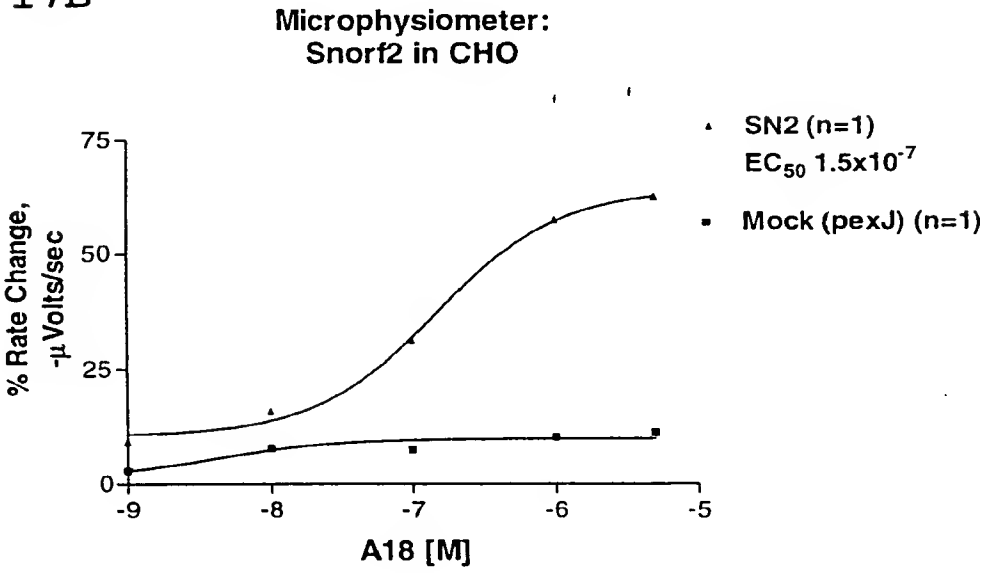


Figure 18A

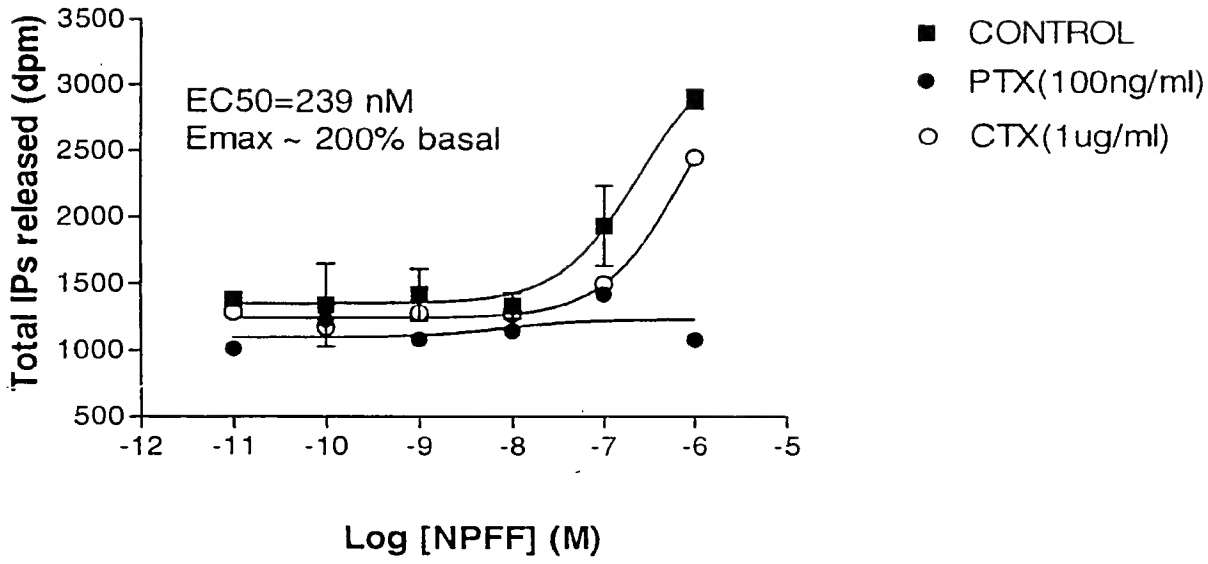


Figure 18B

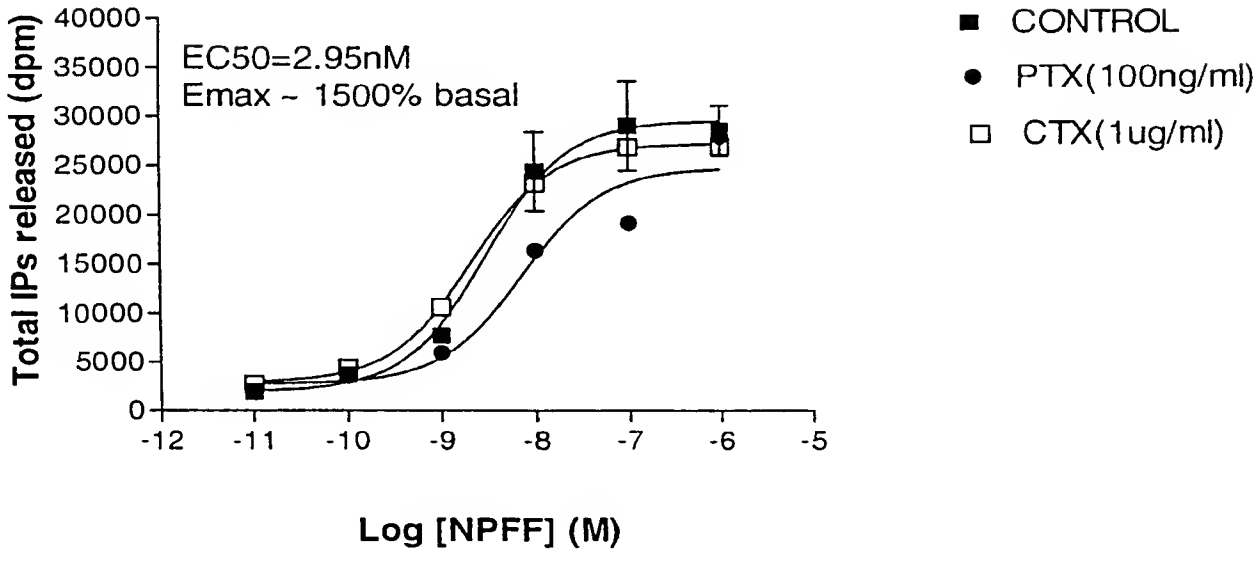


Figure 19

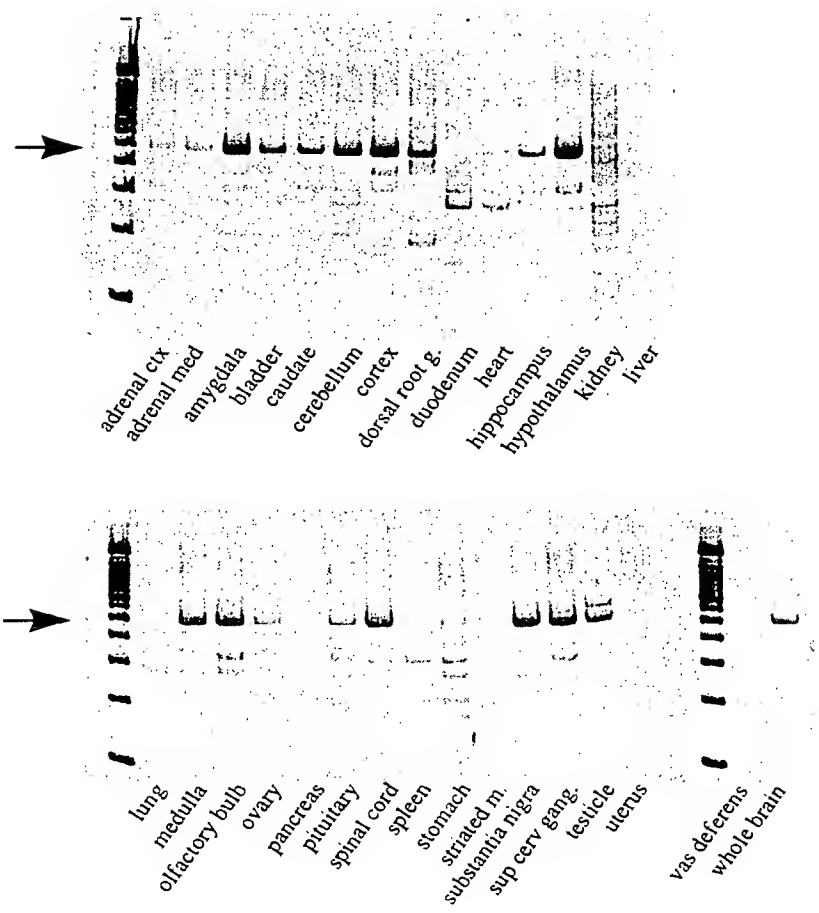

adrenal ctx
adrenal med
amygdala
bladder
caudate
cerebellum
cortex
dorsal root g.
duodenum
heart
hippocampus
hypothalamus
kidney
liver
lung
medulla
olfactory bulb
ovary
pancreas
pituitary
spinal cord
spleen
stomach
striated m.
substantia nigra
sup cerv gang.
testicle
uterus
vas deferens
whole brain

Figure 20

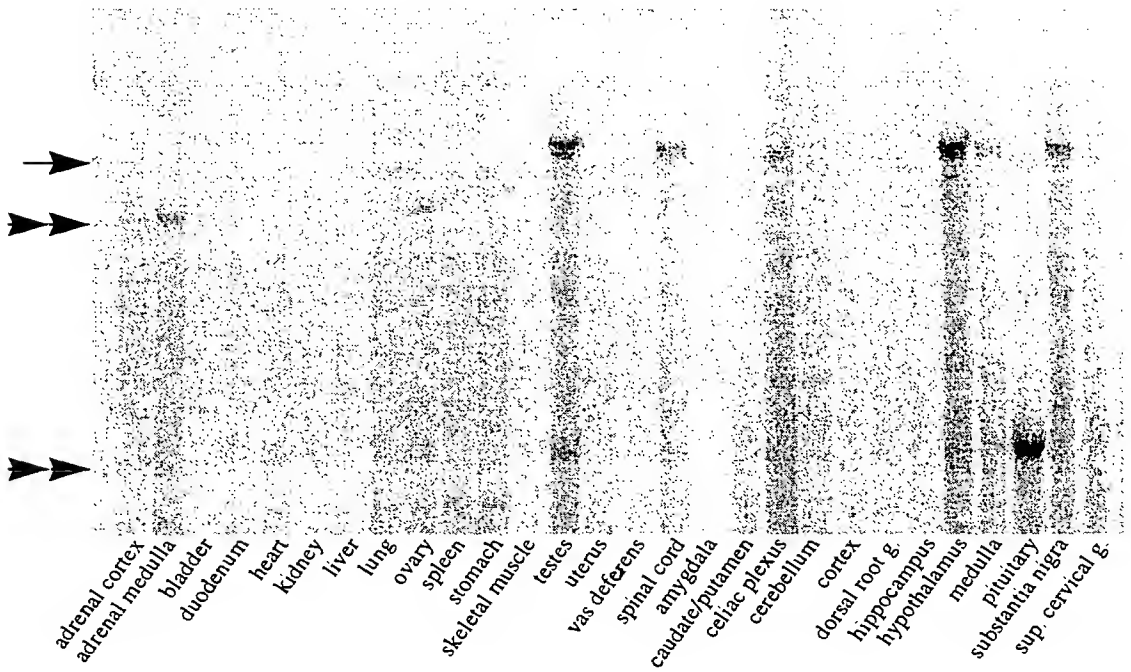
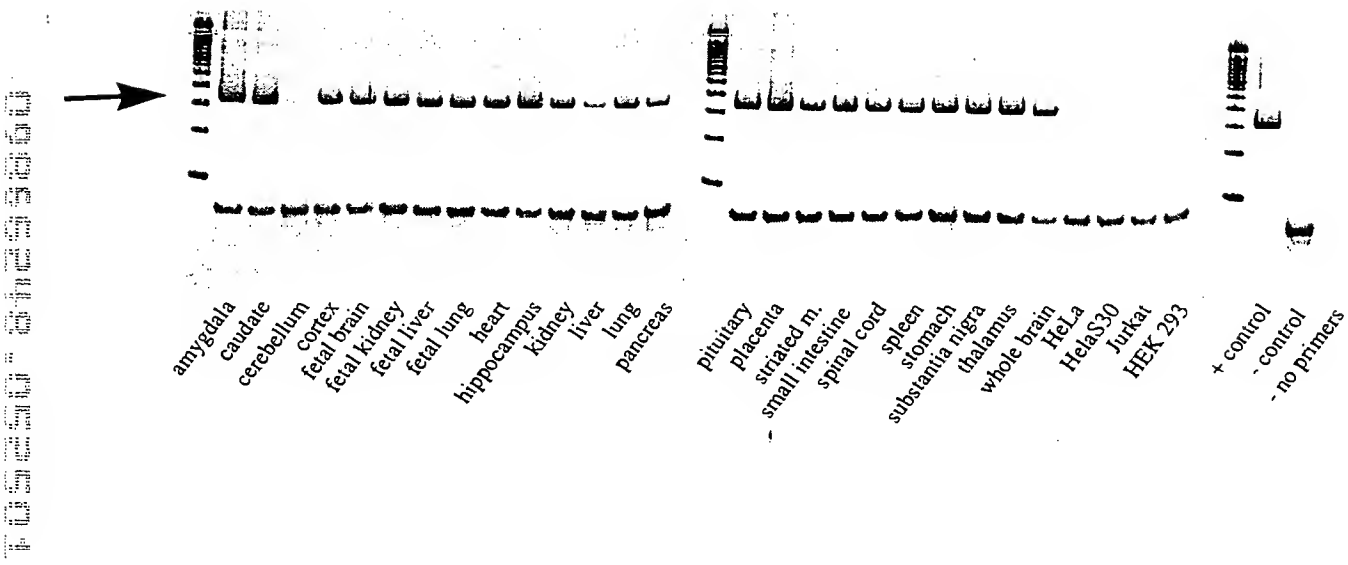

adrenal cortex
adrenal medulla
bladder
duodenum
heart
kidney
liver
lung
ovary
spleen
stomach
skeletal muscle
testes
uterus
vas deferens
spinal cord
amygdala
caudate/putamen
celiac plexus
cerebellum
cortex
dorsal root g.
hippocampus
hypothalamus
medulla
pituitary
substantia nigra
sup. cervical g.

Figure 21


amygdala
caudate
cerebellum
cortex
fetal brain
fetal kidney
fetal liver
fetal lung
heart
hippocampus
kidney
liver
lung
pancreas
pituitary
placenta
striated m.
small intestine
spinal cord
spleen
stomach
substantia nigra
thalamus
whole brain
HeLa
HelaS30
Jurkat
HEK 293
+ control
- control
- no primers